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PCT09

RAW SEQUENCE LISTING   DATE: 12/21/2001
PATENT APPLICATION: US/09/720,583A   TIME: 13:24:11

Input Set : **A:\MBHB00-1314 SequenceListing.txt**
Output Set: **N:\CRF3\12212001\I720583A.raw**

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 3 <110> APPLICANT: DSM N.V.
 4        POUWELS, Pieter
 5        van LUIJK, Nicole
 6        JORE, Johannes
 7        LUITEN, Rudolf
 9 <120> TITLE OF INVENTION: Propionibacterium Vector
11 <130> FILE REFERENCE: MBHB00-1314
13 <140> CURRENT APPLICATION NUMBER: US 09/720,583A
14 <141> CURRENT FILING DATE: 2000-12-22
16 <150> PRIOR APPLICATION NUMBER: PCT/EP99/04416
17 <151> PRIOR FILING DATE: 1999-06-25
19 <150> PRIOR APPLICATION NUMBER: EP 98305033.7
20 <151> PRIOR FILING DATE: 1998-06-25
22 <160> NUMBER OF SEQ ID NOS: 13
24 <170> SOFTWARE: PatentIn version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 3555
28 <212> TYPE: DNA
29 <213> ORGANISM: Propionibacterium freudenreichii LMG16545
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (273)..(1184)
36 <400> SEQUENCE: 1
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39 gccgcaatgc cgaacacgc cccagccatc ccttggagca ggtggcagcg tcaggggagt 120
41 cggggggatgt ttggcagggg atgtggaaag agagttcgct ttgctcacat ggctcaaccg 180
43 ggtaactaac tgatatgggg tcttcgtcgc ccactttgaa cacgccgagg aatggaccac 240
45 gctgaacgtg actcgcatgc ttcactgcat gt atg gat tcg ttc gag acg ttg     293
46                                       Met Asp Ser Phe Glu Thr Leu
47                                       1               5
49 ttc cct gag agc tgg ctg cca cgc aag ccg ctg gcg tca gcc gag aag     341
50 Phe Pro Glu Ser Trp Leu Pro Arg Lys Pro Leu Ala Ser Ala Glu Lys
51         10              15                  20
53 tct ggg gcg tac cgg cac gtg act cgg cag agg gcg ctg gag ctg cct     389
54 Ser Gly Ala Tyr Arg His Val Thr Arg Gln Arg Ala Leu Glu Leu Pro
55     25              30                  35
57 tac atc gaa gcg aac ccg ttg gtc atg cag tcc ttg gtc atc acc gat     437
58 Tyr Ile Glu Ala Asn Pro Leu Val Met Gln Ser Leu Val Ile Thr Asp
59 40              45                  50                  55
61 cga gat gct tcg gat gct gac tgg gcc gca gac ctc gct ggg ctg cct     485
62 Arg Asp Ala Ser Asp Ala Asp Trp Ala Ala Asp Leu Ala Gly Leu Pro
63              60                  65                  70
65 tca ccg tcc tac gtg tcc atg aac cgt gtc acg acc acc gga cac atc     533
66 Ser Pro Ser Tyr Val Ser Met Asn Arg Val Thr Thr Thr Gly His Ile
67          75                  80                  85
69 gtc tat gcc ttg aag aac cct gtg tgt ctg acc gat gcc gcg cgg cga     581
70 Val Tyr Ala Leu Lys Asn Pro Val Cys Leu Thr Asp Ala Ala Arg Arg
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71        90                95                  100
73 cgg cct atc aac ctg ctc gcc cgc gtc gag cag ggc cta tgc gac gtt    629
74 Arg Pro Ile Asn Leu Leu Ala Arg Val Glu Gln Gly Leu Cys Asp Val
75      105               110                 115
77 ctc ggc ggc gat gca tcc tac ggg cac cgg atc aca aag aac ccg ctc    677
78 Leu Gly Gly Asp Ala Ser Tyr Gly His Arg Ile Thr Lys Asn Pro Leu
79 120               125                 130                 135
81 agc acc gcc cat gcg acc ctc tgg ggc ccc gca gac gcg ctc tac gag    725
82 Ser Thr Ala His Ala Thr Leu Trp Gly Pro Ala Asp Ala Leu Tyr Glu
83                 140                 145                 150
85 ctg cgc gcc ctc gca cac acc ctc gac gag atc cac gca ctg ccg gag    773
86 Leu Arg Ala Leu Ala His Thr Leu Asp Glu Ile His Ala Leu Pro Glu
87            155                 160                 165
89 gca ggg aac ccg cgt cgc aac gtc acc cga tca acg gtc ggc cgc aac    821
90 Ala Gly Asn Pro Arg Arg Asn Val Thr Arg Ser Thr Val Gly Arg Asn
91      170               175                 180
93 gtc acc ctg ttc gac acc acc cgc atg tgg gca tac cgg gcc gtc cgg    869
94 Val Thr Leu Phe Asp Thr Thr Arg Met Trp Ala Tyr Arg Ala Val Arg
95      185               190                 195
97 cac tcc tgg ggc ggc ccg gtc gcc gaa tgg gag cac acc gta ttc gag    917
98 His Ser Trp Gly Gly Pro Val Ala Glu Trp Glu His Thr Val Phe Glu
99 200               205                 210                 215
101 cac atc cac cta ctg aac gag acg atc atc gcc gac gaa ttc gcc aca    965
102 His Ile His Leu Leu Asn Glu Thr Ile Ile Ala Asp Glu Phe Ala Thr
103                 220                 225                 230
105 ggc ccc ctc ggc ttg aac gaa ctt aag cac tta tct cga tcc att tcc   1013
106 Gly Pro Leu Gly Leu Asn Glu Leu Lys His Leu Ser Arg Ser Ile Ser
107            235                 240                 245
109 cga tgg gtc tgg cgc aac ttc acc ccc gaa acc ttc cgc gca cgc cag   1061
110 Arg Trp Val Trp Arg Asn Phe Thr Pro Glu Thr Phe Arg Ala Arg Gln
111            250                 255                 260
113 aaa gcg atc agc ctc cgt gga gca tcc aaa ggc ggc aaa gaa ggc ggc   1109
114 Lys Ala Ile Ser Leu Arg Gly Ala Ser Lys Gly Gly Lys Glu Gly Gly
115      265               270                 275
117 cac aaa ggc ggc att gcc agt ggc gca tca cgg cgc gcc cat acc cgt   1157
118 His Lys Gly Gly Ile Ala Ser Gly Ala Ser Arg Arg Ala His Thr Arg
119 280               285                 290                 295
121 caa cag ttc ttg gag ggt ctc tca tga ccacacgtga acgtctcccc         1204
122 Gln Gln Phe Leu Glu Gly Leu Ser
123                 300
125 cgcaacggct acagcatcgc cgctgctgcg aaaaagctcg gtgtctccga gtccaccgtc 1264
127 aagcggtgga cttccgagcc acgcgaggag ttcgtggccc gcgttgccgc acgccacgcg 1324
129 cggattcgtg agctccgctc ggagggtcag agcatgcgtg cgattgctgc cgaggtcggg 1384
131 gtttccgtgg gcaccgtgca ctacgcgctg aacaagaatc gaactgacgc atgaccgtaa 1444
133 cgccgcacga tgagcatttt cttgatcgtg caccgcttgg cactacgttc gcgtgcggtt 1504
135 gcacagtgcg cgccacgttc ttatcctgcg gccattgtgg ctacagccaa tggggggcat 1564
137 cagcaacgga cgttgaaccc ggtgggcaag tgttactcag gggacatgc ccagtctgcg 1624
139 gcgctcggat tgacggtatg gcagtcgtgc atgcggcccc accgtcaaac tcattcaggt 1684
141 atcagtgaga accctcatgg cacccctcg tgacacgttc tcgttgcgat cagctgctgt 1744
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143 gcgtgcgggc gtgagcgttt ctacgctgcg gcgcaggaaa tcagagcttg aggctgccgg 1804
145 agcgacggta gacccgtccg gttgggtggt gccactgcgt gcactcaagg tcgttttttgg 1864
147 ggtgtcagat gagacctcga atgcgcccgg tcatgacgct gagttagtgg cgcagctgcg 1924
149 ctctgagaac gagttttttac ggcgtcaggt cgagcagcag gcgcgcacga tcgaacggca 1984
151 ggctgaggca cacgcggtgg tctcagcgca gctcacacgg gttggccagc ttgaggccgg 2044
153 cgacgcagca gcaccgacac tggcacccgt tgaaaggccg gctccgcgac ggcggtggtg 2104
155 gcagcgtcgg tagcggtcag gatcgctctg gcgtgacgag tgtgtctggc agtgcgaaca 2164
157 gttgctcgac cagtggcagc agaagcgaga tcgctgcgtg gtgctgttcc tcggtcagtt 2224
159 cgtcgaggac tggcgggtct tgctgcgtcc agccgatcgc ctcggcggcc aaggtcagtt 2284
161 ccaagctgtg ccaacgcaca cgcccctcgg ctgacagctg agtctcgaac tgtgcaactg 2344
163 gaccggccgg aagatgcacg ttgccgaggt cgtgagtggc caagcgcacg tcaaagagtg 2404
165 ctgcttcgta gccgcgcaga aatggcagtg ctcggtcgat tcggatcggc ctgcccaggt 2464
167 acattccggg ccgcttgatg aacgcctccg cgtagaagcg caccgttctc ggcccggcct 2524
169 cgtgatctgt cactgtgcac gctcctctcg atggttctcg acgctaccgg agaccaccga 2584
171 cgttcatgcc cagcgcagcg acctgaaagg accaagccga gttagccgtg ctaaccgtat 2644
173 agcttgctcc gtcgcctctg agggcaacca cctgcgcagc aggtgggcgg cagcccgcgc 2704
175 gcaagcgcct accgggtttg ggcacagccc ataaatcaac gcctccggtg ttgaagcgat 2764
177 cgtgtgtcac gattgctatg cttgctaccc cttcagggtt ttcgtataca caaatcaagt 2824
179 tttttcgtat acgctaatgc catgagtgag catctactgc acggcaagcc cgtcaccaac 2884
181 gagcagattc aggcatgggc agacgaggcc gaggccggat acgacctgcc caaactcccc 2944
183 aagccacggc gcggacgccc gcccgtagga gacggtccgg gcaccgtcgt acccgtgcgt 3004
185 ctcgacgcgg ccaccgttgc cgctctcaca gaacgagcaa cagccgaggg catcacgaac 3064
187 cgttcagacg cgatccgagc cgcagtccac gagtggacac gggttgcctg acctccacga 3124
189 ctcagcacgc aagcactacc aacgagaccg gctcgacgac acggccgtgc tctacgcggc 3184
191 cacccacgtt ctcaactccc ggccactcga cgacgaagac gacccgcgcc gctggctcat 3244
193 gatcggaacc gacccagcag gccgcctact cgaactcgtc gcactgatct acgacgacgg 3304
195 ctacgaactg atcatccacg caatgaaagc ccgcacccaa tacctcgacc agctctaacc 3364
197 aagaaaggaa cctgatgagc gaccagctag acagcgaccg caactacgac ccgatgatct 3424
199 tcgacgtgat gcgcgagacc gcgaaccgcg tcgtcgccac gtacgttgca tgggaagatg 3484
201 aagccgctga tccccgcgag gctgcgcact ggcaggccga gcgattccgc acccggcacg 3544
203 aggtgcgcgc c                                                       3555
206 <210> SEQ ID NO: 2
207 <211> LENGTH: 303
208 <212> TYPE: PRT
209 <213> ORGANISM: Propionibacterium freudenreichii LMG16545
211 <400> SEQUENCE: 2
212 Met Asp Ser Phe Glu Thr Leu Phe Pro Glu Ser Trp Leu Pro Arg Lys
213 1               5                   10                  15
215 Pro Leu Ala Ser Ala Glu Lys Ser Gly Ala Tyr Arg His Val Thr Arg
216             20                  25                  30
218 Gln Arg Ala Leu Glu Leu Pro Tyr Ile Glu Ala Asn Pro Leu Val Met
219         35                  40                  45
221 Gln Ser Leu Val Ile Thr Asp Arg Asp Ala Ser Asp Ala Asp Trp Ala
222     50                  55                  60
224 Ala Asp Leu Ala Gly Leu Pro Ser Pro Ser Tyr Val Ser Met Asn Arg
225 65                  70                  75                  80
227 Val Thr Thr Thr Gly His Ile Val Tyr Ala Leu Lys Asn Pro Val Cys
228             85                  90                  95
230 Leu Thr Asp Ala Ala Arg Arg Arg Pro Ile Asn Leu Leu Ala Arg Val
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231              100              105              110
233 Glu Gln Gly Leu Cys Asp Val Leu Gly Gly Asp Ala Ser Tyr Gly His
234          115              120              125
236 Arg Ile Thr Lys Asn Pro Leu Ser Thr Ala His Ala Thr Leu Trp Gly
237      130              135              140
239 Pro Ala Asp Ala Leu Tyr Glu Leu Arg Ala Leu Ala His Thr Leu Asp
240 145              150              155              160
242 Glu Ile His Ala Leu Pro Glu Ala Gly Asn Pro Arg Arg Asn Val Thr
243              165              170              175
245 Arg Ser Thr Val Gly Arg Asn Val Thr Leu Phe Asp Thr Thr Arg Met
246          180              185              190
248 Trp Ala Tyr Arg Ala Val Arg His Ser Trp Gly Gly Pro Val Ala Glu
249          195              200              205
251 Trp Glu His Thr Val Phe Glu His Ile His Leu Leu Asn Glu Thr Ile
252      210              215              220
254 Ile Ala Asp Glu Phe Ala Thr Gly Pro Leu Gly Leu Asn Glu Leu Lys
255 225              230              235              240
257 His Leu Ser Arg Ser Ile Ser Arg Trp Val Trp Arg Asn Phe Thr Pro
258          245              250              255
260 Glu Thr Phe Arg Ala Arg Gln Lys Ala Ile Ser Leu Arg Gly Ala Ser
261          260              265              270
263 Lys Gly Gly Lys Glu Gly Gly His Lys Gly Gly Ile Ala Ser Gly Ala
264          275              280              285
266 Ser Arg Arg Ala His Thr Arg Gln Gln Phe Leu Glu Gly Leu Ser
267      290              295              300
270 <210> SEQ ID NO: 3
271 <211> LENGTH: 85
272 <212> TYPE: PRT
273 <213> ORGANISM: Propionibacterium freudenreichii LMG16545
275 <400> SEQUENCE: 3
276 Met Thr Thr Arg Glu Arg Leu Pro Arg Asn Gly Tyr Ser Ile Ala Ala
277  1               5               10              15
279 Ala Ala Lys Lys Leu Gly Val Ser Glu Ser Thr Val Lys Arg Trp Thr
280          20              25              30
282 Ser Glu Pro Arg Glu Glu Phe Val Ala Arg Val Ala Ala Arg His Ala
283          35              40              45
285 Arg Ile Arg Glu Leu Arg Ser Glu Gly Gln Ser Met Arg Ala Ile Ala
286      50              55              60
288 Ala Glu Val Gly Val Ser Val Gly Thr Val His Tyr Ala Leu Asn Lys
289 65              70              75              80
291 Asn Arg Thr Asp Ala
292              85
295 <210> SEQ ID NO: 4
296 <211> LENGTH: 59
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Synthetic Duplex DNA designed to link EcoRI and AvaI
303 <400> SEQUENCE: 4
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RAW SEQUENCE LISTING   DATE: 12/21/2001
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Input Set : A:\MBHB00-1314 SequenceListing.txt
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304 aattcaagct tgtcgacgtt aacctgcagg catgcggatc cggtaccgat atcagatct  59
307 <210> SEQ ID NO: 5
308 <211> LENGTH: 59
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Synthetic Duplex DNA designed to link EcoRI and AvaI
315 <400> SEQUENCE: 5
316 ccgaagatct gatatcggta ccggatccgc atgcctgcag gttaacgtcg acaagcttg  59
319 <210> SEQ ID NO: 6
320 <211> LENGTH: 24
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Synthetic DNA designed to create Acc65I and BglII ends
327 <400> SEQUENCE: 6
328 gtaccggccg ctgcggccaa gctt                                        24
331 <210> SEQ ID NO: 7
332 <211> LENGTH: 24
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Synthetic DNA designed to create Acc65I and BglII ends
339 <400> SEQUENCE: 7
340 gatcaagctt ggccgcagcg gccg                                        24
343 <210> SEQ ID NO: 8
344 <211> LENGTH: 35
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Synthetic primer for erythromycin resistance
351 <400> SEQUENCE: 8
352 aaactgcagc tgctggcttg cgcccgatgc tagtc                            35,
355 <210> SEQ ID NO: 9
356 <211> LENGTH: 76
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial Sequence
360 <220> FEATURE:
361 <223> OTHER INFORMATION: Synthetic primer for erythromycin resistance
363 <400> SEQUENCE: 9
364 aaactgcagc agctgggcag gccgctggac ggcctgccct cgagctcgtc tagaatgtgc 60
366 tgccgatcct ggttgc                                                 76
369 <210> SEQ ID NO: 10
370 <211> LENGTH: 32
371 <212> TYPE: DNA
372 <213> ORGANISM: Artificial Sequence
374 <220> FEATURE:
375 <223> OTHER INFORMATION: Synthetic primer for cobA
377 <400> SEQUENCE: 10
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VERIFICATION SUMMARY   DATE: 12/21/2001
PATENT APPLICATION: US/09/720,583A   TIME: 13:24:12

Input Set : **A:\MBHB00-1314 SequenceListing.txt**
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